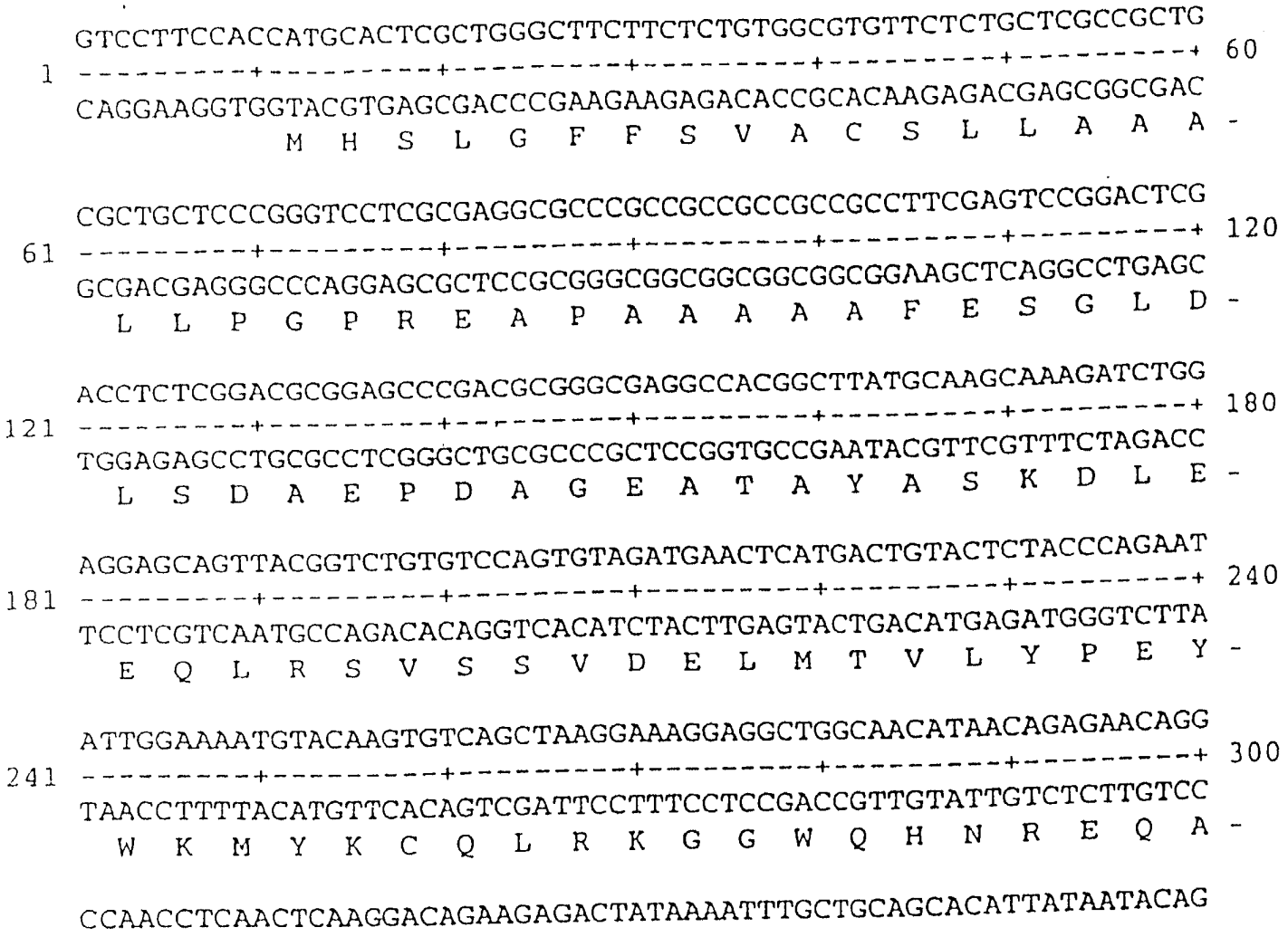
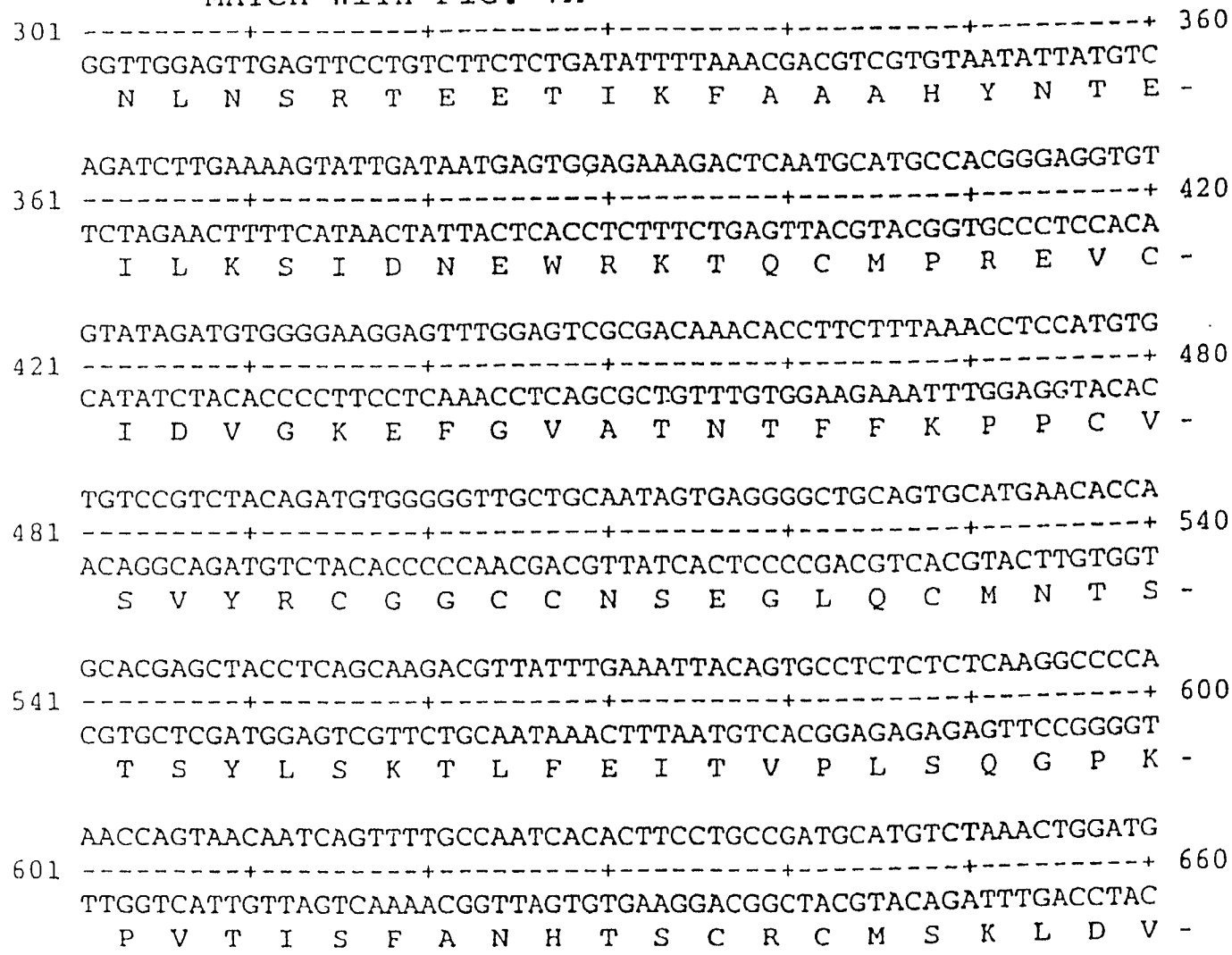


MATCH WITH FIG. 1B

Fig. 1A

MATCH WITH FIG. 1A



MATCH WITH FIG. 1C

Fig. 1B

MATCH WITH FIG. 1B

```
    TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
661 ---------+---------+---------+---------+---------+---------+ 720
    AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTCACAG
      Y  R  Q  V  H  S  I  I  R  R  S  L  P  A  T  L  P  Q  C  Q -

    AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
721 ---------+---------+---------+---------+---------+---------+ 780
    TCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGG
      A  A  N  K  T  C  P  T  N  Y  M  W  N  N  H  I  C  R  C  L -

    TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
781 ---------+---------+---------+---------+---------+---------+ 840
    ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
      A  Q  E  D  F  M  F  S  S  D  A  G  D  D  S  T  D  G  F  H -

    ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
841 ---------+---------+---------+---------+---------+---------+ 900
    TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
      D  I  C  G  P  N  K  E  L  D  E  E  T  C  Q  C  V  C  R  A -

    CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
901 ---------+---------+---------+---------+---------+---------+ 960
    GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCA
      G  L  R  P  A  S  C  G  P  H  K  E  L  D  R  N  S  C  Q  C -

    GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
961 ---------+---------+---------+---------+---------+---------+ 1020
    CACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
```

MATCH WITH FIG. 1D

Fig.1C

MATCH WITH FIG. 1C

```
      V  C  K  N  K  L  F  P  S  Q  C  G  A  N  R  E  F  D  E  N -

      ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
1021  ---------+---------+---------+---------+---------+---------+ 1080
      TGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTT
        T  C  Q  C  V  C  K  R  T  C  P  R  N  Q  P  L  N  P  G  K -

      AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
1081  ---------+---------+---------+---------+---------+---------+ 1140
      TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTTCTTCAAGG
        C  A  C  E  C  T  E  S  P  Q  K  C  L  L  K  G  K  K  F  H -

      ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC
1141  ---------+---------+---------+---------+---------+---------+ 1200
      TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
        H  Q  T  C  S  C  Y  R  R  P  C  T  N  R  Q  K  A  C  E  P -

      CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
1201  ---------+---------+---------+---------+---------+---------+ 1260
      GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
        G  F  S  Y  S  E  E  V  C  R  C  V  P  S  Y  W  Q  R  P  Q -

      AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT
```

MATCH WITH FIG. 1E

Fig. 1D

MATCH WITH FIG. 1D

```
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
       M   S   *

     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT

     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

     CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCGGTTCTAAAAGGAG

     TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTTATAACAAAGACG

     ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA

     GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAAA
1621 ---------+---------+---------+---------+---------+---- 1674
     CGTTTTATACAAATTTTATTTTACTTTTAACATAAATATTTTTTTTTTTTTTTT
```

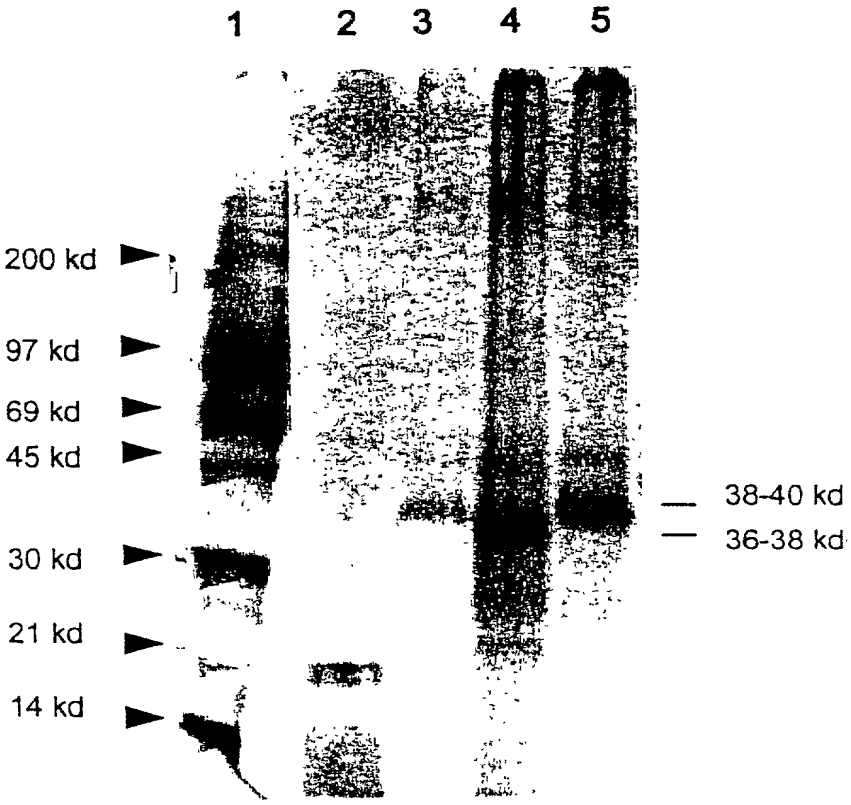
Fig. 1E

```
      1                                                  50
Pdgfa .MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdgfb MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH
 Vegf .....MNFLL SWVHWSLALL LY..... ..... .LHHAKWSQA
Vegf2 .......MTV LYPEYWKMYK CQ..... ..... .LRKGGWQHN

      51                                                 100
Pdgfa IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP
Pdgfb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
 Vegf APMAE..... ......GGGQ NHHEVVKFMD .VYQR..... .....
Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK..... .....

      101                                                150
Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS
Pdgfb AECKTRTEVF EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT
 Vegf SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2 TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

      151                                                200
Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECACA.... AT.....
Pdgfb QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKCA.... ETVAAARPVT
 Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII
```

Fig. 2A

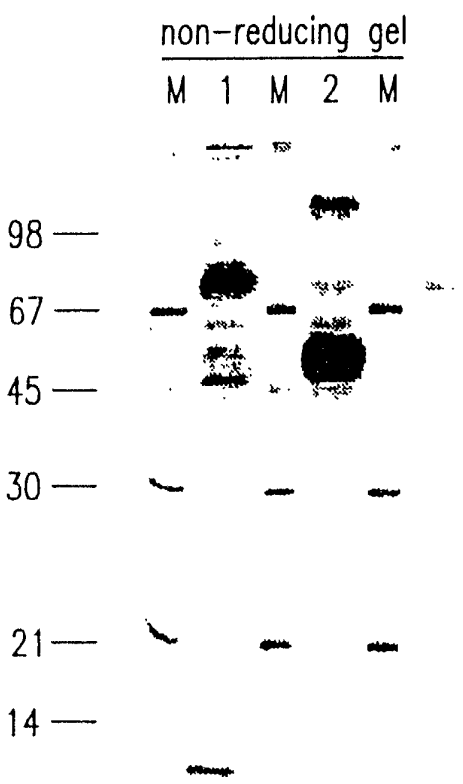
```
      201                                                        250
Pdgfa ....TSLNPD YREEDTDVR. ..... ..... .....
Pdgfb RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG
 Vegf RGK..... .GKGQKRKRK KSRYKSWSVY VGARCCLMPW SLPGPHP...
Vegf2 RRSLPATLPQ CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG

      251                                                        300
Pdgfa ..... ..... ..... ..... .....
Pdgfb A..... ..... ..... ..... .....
 Vegf ....CGP... ..... .....CSE RRKHLFVQDP QTCKCSCKNT
Vegf2 FHDICGPNKE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

      301                                                        350
Pdgfa ..... ..... ..... ..... .....
Pdgfb ..... ..... ..... ..... .....
 Vegf ..DSRCKARQ LELNERTCRC DKPRR..... ..... .....
Vegf2 LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL

      351                                                        398
Pdgfa ..... ..... ..... ..... .....
Pdgfb ..... ..... ..... ..... .....
 Vegf ..... ..... ..... ..... .....
Vegf2 KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS
```

Fig. 2B

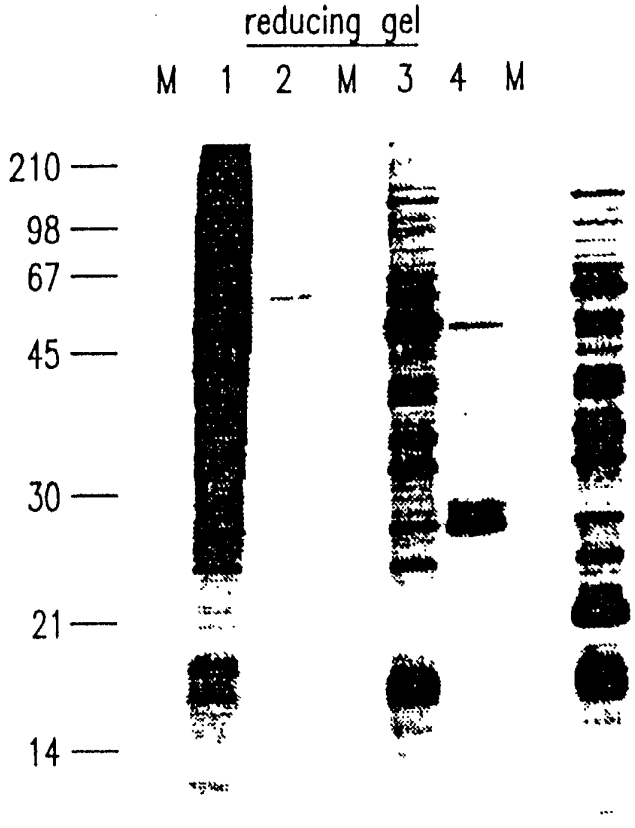


Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse $ forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

Fig. 3

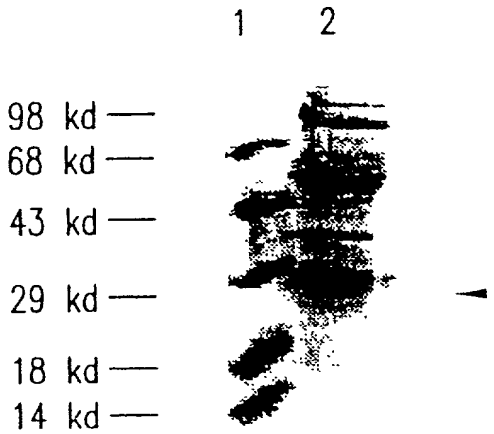


Lane M Marker
Lane 1 vector medium
Lane 2 VEGF2 medium



Lane M: Marker
Lane 1: vector Cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 Cytoplasm
Lane 4: VEGF2 medium

Fig. 4



Lane 1: Molelular weight marker
Lane 2: Precipitates containing VEGF2.

Fig. 5

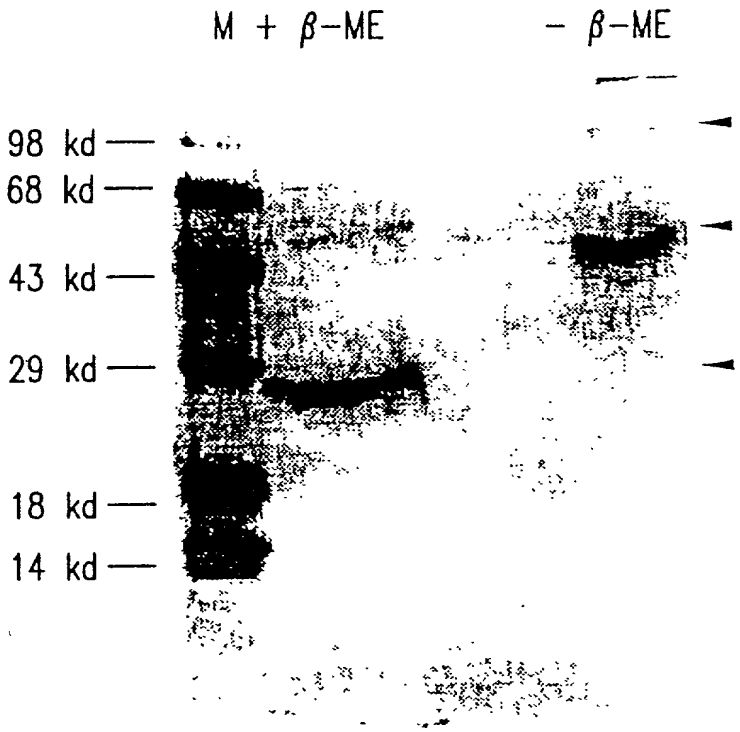


Fig. 6

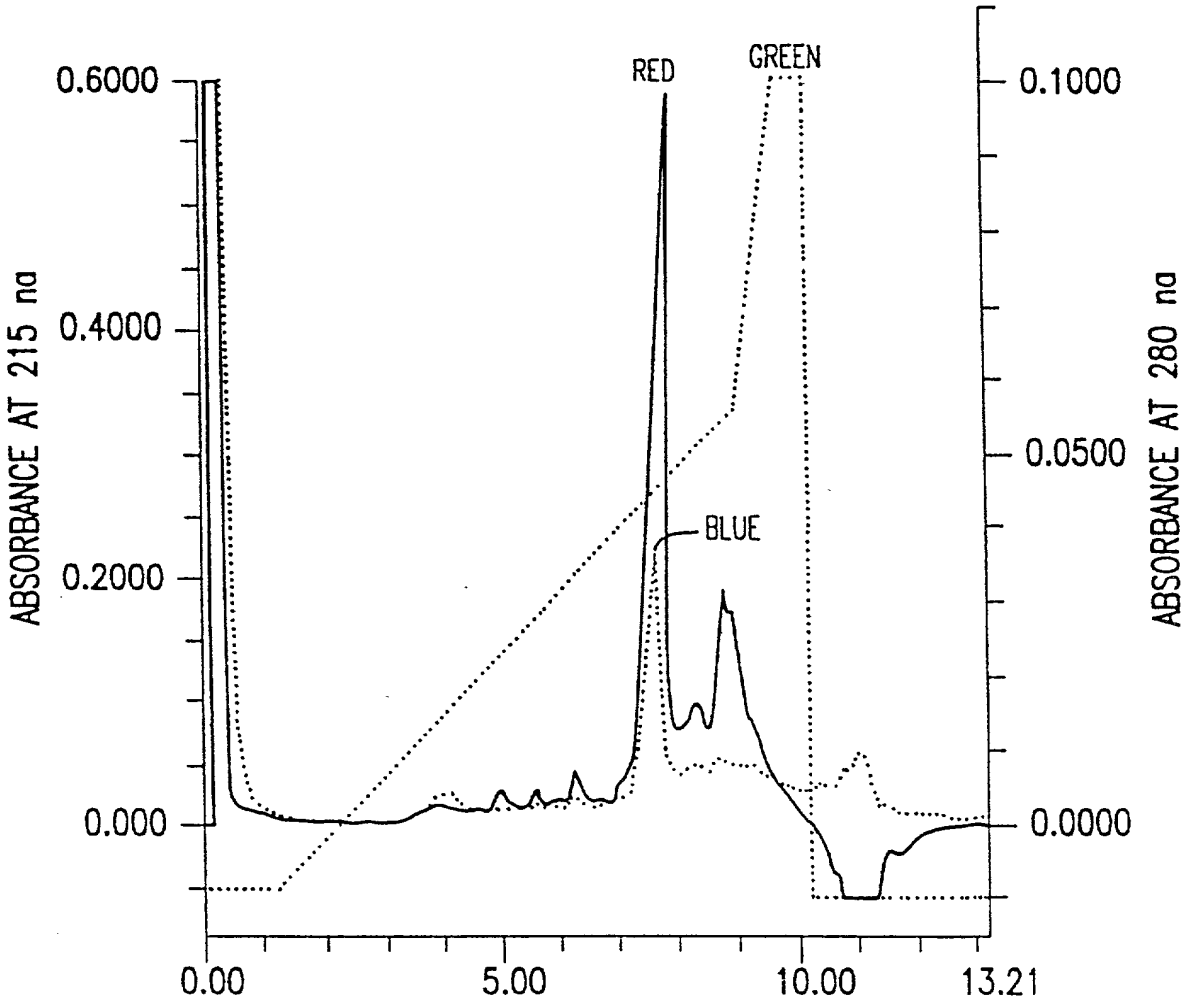

0.6000
0.4000
0.2000
0.000
ABSORBANCE AT 215 nm
0.1000
0.0500
0.0000
ABSORBANCE AT 280 nm
RED
GREEN
BLUE
0.00
5.00
10.00
13.21

Fig. 7

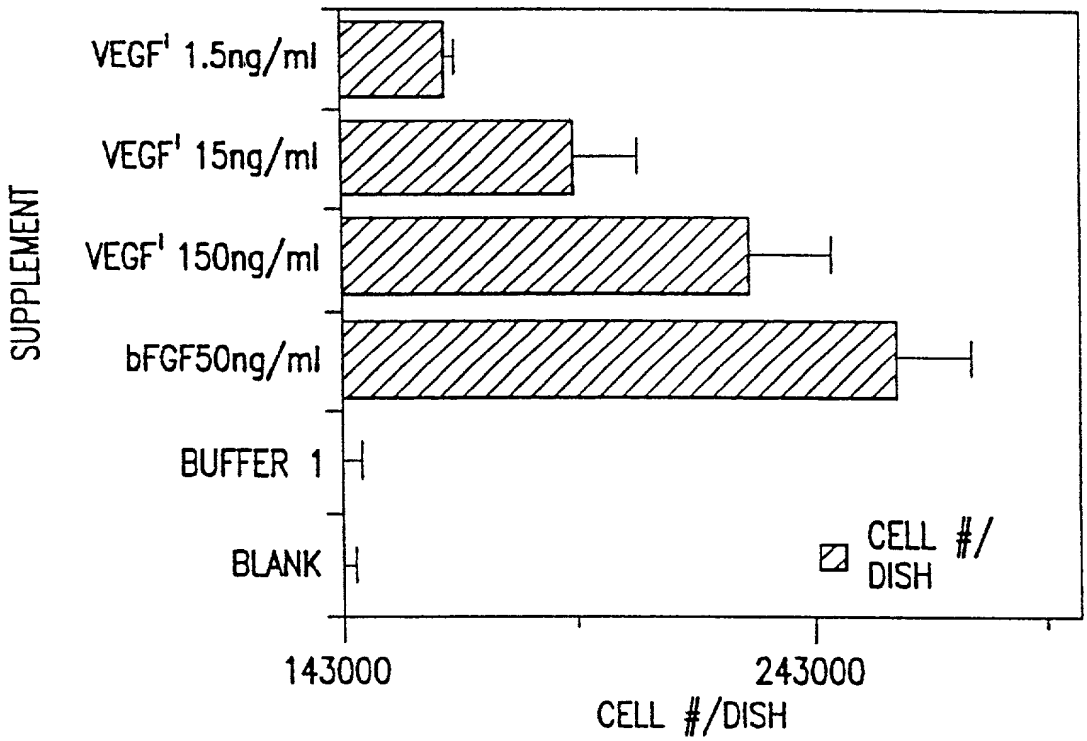

VEGF' 1.5ng/ml
VEGF' 15ng/ml
VEGF' 150ng/ml
bFGF50ng/ml
BUFFER 1
BLANK
SUPPLEMENT
CELL #/ DISH
143000
243000
CELL #/DISH

Fig. 8

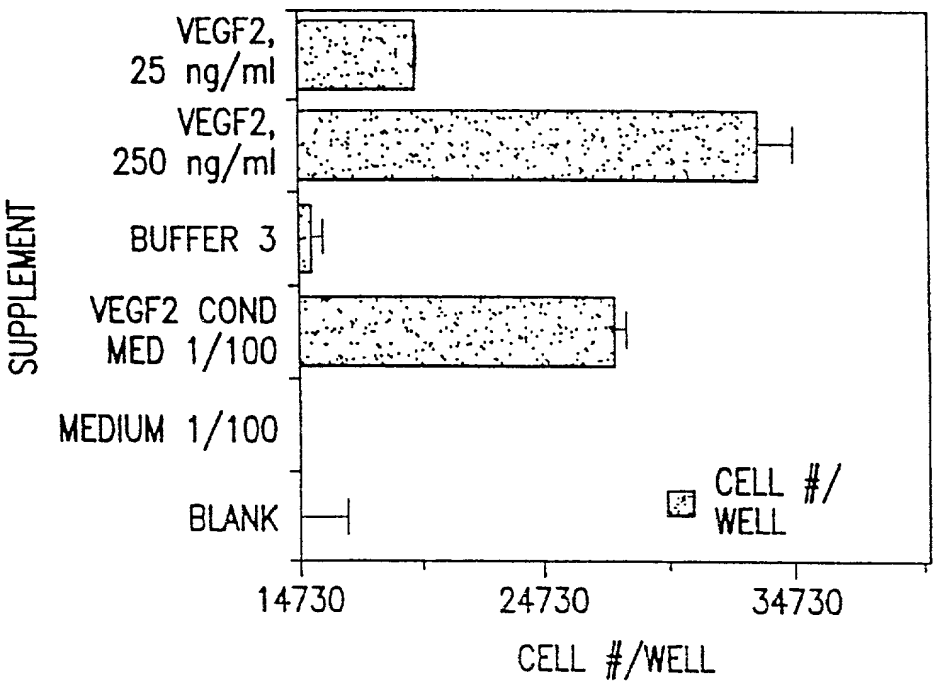

VEGF2,
25 ng/ml
VEGF2,
250 ng/ml
BUFFER 3
VEGF2 COND
MED 1/100
MEDIUM 1/100
BLANK
SUPPLEMENT
CELL #/
WELL
14730
24730
34730
CELL #/WELL

Fig. 9